

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lal, Preeti  
Guegler, Karl J.  
Corley, Neil C.

(ii) TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
(B) STREET: 3174 PORTER DRIVE  
(C) CITY: PALO ALTO  
(D) STATE: CALIFORNIA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CERRONE, MICHAEL C.  
(B) REGISTRATION NUMBER: 39,132  
(C) REFERENCE/DOCKET NUMBER: PF-0527 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 855-0555  
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSTUT10  
(B) CLONE: 1691243

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met	Val	His	Val	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser
											5	10	15	
Glu	Arg	Tyr	Leu	Phe	Leu	Asn	Met	Ala	Tyr	Gln	Gln	Val	His	Ala
											20	25	30	
Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu	Val	Trp	Arg	Ile	Glu
											35	40	45	
Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu	Ser	Leu
											50	55	60	
Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp
											65	70	75	
Arg	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu
											80	85	90	
Leu	Ile	Ser	Thr	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala
											95	100	105	
Phe	Glu	Glu	Tyr	Tyr	Arg	Phe	Tyr	Thr	Pro	Pro	Asn	Phe	Val	
											110	115	120	
Leu	Ala	Leu	Val	Leu	Pro	Ser	Ile	Val	Ile	Leu	Asp	Leu	Leu	Gln
											125	130	135	
Leu	Cys	Arg	Tyr	Pro	Asp									
											140			

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Phe	Leu	Pro	Pro	Val	Val	Leu	Ala	Ile	Arg	Ser	Arg	Tyr	Val
											5	10	15	
Leu	Glu	Ala	Ala	Val	Tyr	Thr	Phe	Thr	Met	Phe	Phe	Ser	Thr	Phe
											20	25	30	
Tyr	His	Ala	Cys	Asp	Gln	Pro	Gly	Ile	Val	Val	Phe	Cys	Ile	Met
											35	40	45	
Asp	Tyr	Asp	Val	Leu	Gln	Phe	Cys	Asp	Phe	Leu	Gly	Ser	Leu	Met
											50	55	60	
Ser	Val	Trp	Val	Thr	Val	Ile	Ala	Met	Ala	Arg	Leu	Gln	Pro	Val
											65	70	75	
Val	Lys	Gln	Val	Leu	Tyr	Leu	Leu	Gly	Ala	Met	Leu	Leu	Ser	Met
											80	85	90	
Ala	Leu	Gln	Leu	Asp	Arg	His	Gly	Leu	Trp	Asn	Leu	Leu	Gly	Pro
											95	100	105	
Ser	Leu	Phe	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Ala	Trp	Thr	Val	Arg
											110	115	120	
Ser	Val	Arg	Arg	Arg	His	Cys	Tyr	Pro	Pro	Thr	Trp	Arg	Arg	Trp
											125	130	135	
Leu	Phe	Tyr	Leu	Cys	Pro	Gly	Ser	Leu	Ile	Ala	Gly	Ser	Ala	Val
											140	145	150	
Leu	Leu	Tyr	Ala	Phe	Val	Glu	Thr	Arg	Asp	Asn	Tyr	Phe	Tyr	Ile

155	160	165
His Ser Ile Trp His Met Leu Ile Ala	Gly Ser Val Gly Phe	Leu
170	175	180
Leu Pro Pro Arg Ala Lys Thr Asp His	Gly Val Pro Ser Gly	Ala
185	190	195
Arg Ala Arg Gly Cys Gly Tyr Gln Leu	Cys Ile Asn Glu Gln	Glu
200	205	210
Glu Pro Gly Pro Arg Gly Pro Arg Arg	Gly His Cys Gln Gln	His
215	220	225
Leu Cys Gln Leu Arg Gly Ala Leu Gly	Leu Ala Leu Arg Gly	Tyr
230	235	240
Glu Cys Phe Leu Glu Phe Leu Gly	Val Trp Ser Pro Leu	Arg
245	250	255
Arg Arg Gln Ala Val Phe Leu Glu Asp	Met Glu Ser Phe Ser	Arg
260	265	270
Thr Gln Asn Ser Ser Arg Asp Leu Glu	Pro Phe Pro Gly His	Gly
275	280	285
Glu Leu Pro Glu Gly Leu Glu Ser Pro	Cys Ile Met Glu Ser	Phe
290	295	300
Leu Arg Thr Gly Ala Tyr Ala Gly Thr	Glu Ser Leu Arg Thr	Lys
305	310	315
Glu Ser Leu Leu Gln Val Trp Ser Leu	Ser Trp Asp Ala Glu	Pro
320	325	330
Ser Gln Asp Met Asp Ser Phe Pro Gly	Arg Gln Ser Pro Val	Arg
335	340	345
Ser Thr Ala Ser Phe Gln Arg Arg Trp	Ser Leu Ser Trp Gly	Asn
350	355	360
Gln Ile Ser Arg Phe Ser Gln Arg Leu	Ser Asn Ser Gly Leu	Arg
365	370	375
Leu Pro Ser Gln Arg Gln Arg Leu Gly	Cys Ala Val Leu Trp	Arg
380	385	390
Arg Asp Cys Arg Met Asp Gly Ala Gly	Thr Gly Ala Val Trp	Val
395	400	405
Ala Gly Ile Leu Val		
410		

## (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT10
- (B) CLONE: 1691243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

CAAGTATAAGG AGATTCCAC CTTGGTTGGA AACCTGGTTA CAGTGTAGAA AACAGCTTGG 60  
ATTACTAAGT TTTTCTTCG CTATGGTCCA TGTTGCCTAC AGCCTCTGCT TACCGATGAG 120  
AACGTCAGAG AGATATTTGT TTCTCAACAT GGCTTATCAG CAGGTTCATG CAAATATTGA 180  
AAACTCTTGG AATGAGGAAG AAGTTGGAG AATTGAAATG TATATCTCCT TTGGCATAAT 240  
GAGCCTTGGC TTACTTCCC TCCTGGCAGT CACTTCTATC CCTTCAGTGA GCAATGCTTT 300  
AAACTGGAGA GAATTCAGTC TTATTCAGTC TACACTTGGA TATGTCGCTC TGCTCATAAG 360  
TACTTTCCAT GTTTAATTG ATGGATGGAA ACGAGCTTT GAGGAAGAGT ACTACAGATT 420  
TTATACACCA CCAAACTTG TTCTTGCTCT TGTTTGCCC TCAATTGTAA TTCTGGATCT 480

TTTGCAGCTT TGCAGATACC CAGACTGAGC TGGAACCTGGA ATTTGTCTTC CTATTGACTC 540  
 TACTTCTTAA AAAGCGGCTG CCCATTACAT TCCTCAGCTG TCCTTGCACT TAGGTGTACA 600  
 TGTGACTGAG TGTTGCCAG TGAGATGAAG TCTCCTCAAA GGAAGGCAGC ATGTGTCCTT 660  
 TTTCATCCCT TCATCTTGCT GCTGGGATTG TGGATATAAC AGGAGCCCTG GCAGCTGTCT 720  
 CCAGAGGATC AAAGCCACAC CCAAAGAGTA AGGCAGATTAGAGACCAAGAAGACCTTGAC 780  
 TACTTCCCTA CTTCCACTGC TTTTCTCCTGC ATTTAAGCCA TTGTAATCTTGGGTGTGTTA 840  
 CATGAAGTGA AAATTAATTTC TTTCTGCCCT TCAGTTCTTT ATCCTGATAC CATTAAACAC 900  
 TGTCTGAATT AACTAGACTG CAATAATTCT TTCTTTGAA AGCTTTAAA GGATAATGTG 960  
 CAATTACAT TAAAATTGAT TTTCCATTGAT CAATTAGTTA TACTCATTTC CCTGCCTTGA 1020  
 TCTTTCATTA GATATTTTGAT ATCTGCTTGG AATATATTAT CTTCTTTTA ACTGTGTAAT 1080  
 TGGTAATTAC TAAAACCTCTG TAATCTCCAA AATATGCTA TCAAATTACA CACCATGTTT 1140  
 TCTATCATTC TCATAGATCT GCCTTATAAA CATTAAATA AAAAGTACTA TTTAATGATT 1200  
 TAAAAAAA AAA 1213

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1297 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: BRSTTUT03  
 (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

CGGACGGCGTG GGCTGCTCTG CCTGAGCAAC CTCATGTTTC TGCCACCTGT GGTCCCTGGCC 60  
 ATTGCGAGTC GATATGTGCT GGAAGCTGCA GTCTACACCT TCACCATGTT CTTCTCCACG 120  
 TTCTATCATG CCTGTGACCA GCCAGGCATC GTGGTTTCT GCATCATGGA CTACGATGTG 180  
 CTGCACTTCT GTGATTTCCT GGGCTCTTA ATGTCCGTGT GGGTCACTGT CATTGCCATG 240  
 GCTCGTTAC AGCCCGTGGT CAAGCAGGTG CTGTATTGTC TGGGAGCTAT GCTGCTGTCC 300  
 ATGGCTCTGC AGCTTGACCG ACATGGACTC TGGAACCTGC TTGGACCCAG TCTCTCGCC 360  
 CTGGGGATCT TGGCACAGC CTGGACAGTA CGCAGCGTCC GCGGCCGGCA CTGCTACCCA 420  
 CCCACGTGGC GCGCCTGGCT TTTCTACTTG TGCCCTGGCA GCCTTATTGTC AGGCAGTGCC 480  
 GTCCTGCTT ATGCTTTGAT GGAGACCCGG GACAACACT TCTACATTCA CAGCATTGG 540  
 CATATGCTCA TTGCGGGCAG TGTGGGCTTC CTGCTGCCCT CTCGTGCCAA GACTGACCAC 600  
 GGGGTCCCAT CTGGAGCCCG GGCCCGGGGC TGTGGTTACC AGCTATGCAT CAACGAGCAG 660  
 GAGGAGCCTG GGCCTCGTGG GCCCAGGAGG GGCCACTGTC AGCAGCATCT GTGCCAGCTG 720  
 AGAGGGGCTT TGGGCTCTGGC CCTGAGGGGA TATGAATGCT TCCTAGAGTT CTTCTGGGG 780  
 GTGTGGAGGC CTCTTAGAAG GAGACAGGGT GTATTCTTG AGGACATGGT GTCTTCTCA 840  
 AGGACACAAA ACTCTTCCAG GGACCTGGAG CCCTTCCCAG GACATGGAGA ACTTCCTGAG 900  
 GGCCTGGAGT CCCCTGCAT CATGGAGTCC TTCTTAAGGA CTGGAGCCTA TGCAGGCACA 960  
 GAGTCCCTCA GGACCAAGGA GTCCCTCCTG CAGGTGGGA GCCTTCCCTG GGATGCAGAG 1020  
 CCTTCCCAAG ACATGGATTG CTTCCCAGGG AGACAAAGCC CTGTCAGGAG CACAGCATCT 1080  
 TTCCAGAGGA GGTGGAGTCT ATCTTGGGGAA AACCAAATT CCAGATTTTC CCAGAGGCTC 1140  
 AGCAACTCTG GCCTCAGGCT TCCTTCCCAAG AGGCAGCGTC TGGGCTGTGTC TGTGCTGTGG 1200  
 AGGAGGGATT GCAGGATGGA TGGAGCTGGG ACTGGGGCTG TCTGGGTGGC TGGTATCCTC 1260  
 GTTTGATACA GGTGGAGTCT CTGTGCTCC ATAGAAG 1297

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: GenBank  
 (B) CLONE: 1216498

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met	Gly	Arg	Ala	Met	Val	Val	Arg	Leu	Gly	Leu	Leu	Leu		
				5				10				15		
Leu	Ala	Leu	Leu	Leu	Pro	Thr	Gln	Ile	Tyr	Cys	Asn	Gln	Thr	Ser
				20				25				30		
Val	Ala	Pro	Phe	Ser	Gly	Asn	Gln	Ser	Ile	Ser	Ala	Ala	Pro	Asn
				35				40				45		
Pro	Thr	Asn	Ala	Thr	Thr	Arg	Ser	Gly	Cys	Ser	Ser	Leu	Gln	Ser
				50				55				60		
Thr	Ala	Gly	Leu	Leu	Ala	Leu	Ser	Leu	Ser	Leu	Leu	His	Leu	Tyr
				65				70				75		
														Cys

## (2) INFORMATION FOR SEQ ID NO: 6 :

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: GenBank  
 (B) CLONE: 130989

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met	Trp	Val	Pro	Val	Val	Phe	Leu	Thr	Leu	Ser	Val	Thr	Trp	Ile
				5				10					15	
Gly	Ala	Ala	Pro	Leu	Ile	Leu	Ser	Arg	Ile	Val	Gly	Gly	Trp	Glu
				20				25					30	
Cys	Glu	Lys	His	Ser	Gln	Pro	Trp	Gln	Val	Leu	Val	Ala	Ser	Arg
				35				40					45	
Gly	Arg	Ala	Val	Cys	Gly	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val
				50				55					60	
Leu	Thr	Ala	Ala	His	Cys	Ile	Arg	Asn	Lys	Ser	Val	Ile	Leu	Leu
				65				70					75	
Gly	Arg	His	Ser	Leu	Phe	His	Pro	Glu	Asp	Thr	Gly	Gln	Val	Phe
				80				85					90	
Gln	Val	Ser	His	Ser	Phe	Pro	His	Pro	Leu	Tyr	Asp	Met	Ser	Leu
				95				100					105	
Leu	Lys	Asn	Arg	Phe	Leu	Arg	Pro	Gly	Asp	Asp	Ser	Ser	His	Asp
				110				115					120	
Leu	Met	Leu	Leu	Arg	Leu	Ser	Glu	Pro	Ala	Glu	Leu	Thr	Asp	Ala
				125				130					135	
Val	Lys	Val	Met	Asp	Leu	Pro	Thr	Gln	Glu	Pro	Ala	Leu	Gly	Thr
				140				145					150	
Thr	Cys	Tyr	Ala	Ser	Gly	Trp	Gly	Ser	Ile	Glu	Pro	Glu	Glu	Phe
				155				160					165	
Leu	Thr	Pro	Lys	Lys	Leu	Gln	Cys	Val	Asp	Leu	His	Val	Ile	Ser
				170				175					180	
Asn	Asp	Val	Cys	Ala	Gln	Val	His	Pro	Gln	Lys	Val	Thr	Lys	Phe
				185				190					195	

Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Thr Cys Ser  
 200 205 210  
 Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln Gly  
 215 220 225  
 Ile Thr Ser Trp Gly Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro  
 230 235 240  
 Ser Leu Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp  
 245 250 255  
 Thr Ile Val Ala Asn Pro  
 260

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1317 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: GenBank
  - (B) CLONE: 2459993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met Leu Ala Cys Leu Cys Cys Lys Lys Gly Gly Ile Gly Phe Lys  
 5 10 15  
 Glu Phe Glu Asn Ala Glu Gly Asp Glu Tyr Val Ala Asp Phe Ser  
 20 25 30  
 Glu Gln Gly Ser Pro Ala Ala Ala Gln Thr Gly Pro Asp Val  
 35 40 45  
 Tyr Val Leu Pro Leu Thr Glu Val Ser Leu Pro Met Ala Lys Gln  
 50 55 60  
 Pro Gly Arg Ser Val Gln Leu Leu Lys Ser Thr Asp Leu Gly Arg  
 65 70 75  
 His Ser Leu Leu Tyr Leu Lys Glu Ile Gly His Gly Trp Phe Gly  
 80 85 90  
 Lys Val Phe Leu Gly Glu Val His Ser Gly Val Ser Gly Thr Gln  
 95 100 105  
 Val Val Val Lys Glu Leu Lys Val Ser Ala Ser Val Gln Glu Gln  
 110 115 120  
 Met Gln Phe Leu Glu Ala Gln Pro Tyr Arg Ala Leu Gln His  
 125 130 135  
 Ser Asn Leu Leu Gln Cys Leu Ala Gln Cys Ala Glu Val Thr Pro  
 140 145 150  
 Tyr Leu Leu Val Met Glu Phe Cys Pro Leu Gly Asp Leu Lys Gly  
 155 160 165  
 Tyr Leu Arg Ser Cys Arg Val Thr Glu Ser Met Ala Pro Asp Pro  
 170 175 180  
 Leu Thr Leu Gln Arg Met Ala Cys Glu Val Ala Cys Gly Val Leu  
 185 190 195  
 His Leu His Arg His Asn Tyr Val His Ser Asp Leu Ala Leu Arg  
 200 205 210  
 Asn Cys Leu Leu Thr Ala Asp Leu Thr Val Lys Val Gly Asp Tyr  
 215 220 225  
 Gly Leu Ser His Cys Lys Tyr Arg Glu Asp Tyr Leu Val Thr Ala  
 230 235 240  
 Asp Gln Leu Trp Val Pro Leu Arg Trp Ile Ala Pro Glu Leu Val

245	250	255
Asp Glu Val His Gly Asn Leu Leu Val Val	Asp Gln Thr Lys Ser	
260	265	270
Ser Asn Val Trp Ser Leu Gly Val Thr Ile	Trp Glu Leu Phe Glu	
275	280	285
Leu Gly Ala Gln Pro Tyr Pro Gln His Ser	Asp Arg Gln Val Leu	
290	295	300
Ala Tyr Ala Val Arg Glu Gln Gln Leu Lys	Leu Pro Lys Pro Gln	
305	310	315
Leu Gln Leu Ala Leu Ser Asp Arg Trp Tyr	Glu Val Met Gln Phe	
320	325	330
Cys Trp Leu Gln Pro Glu Gln Arg Pro Thr	Ala Glu Glu Val His	
335	340	345
Leu Leu Leu Ser Tyr Leu Cys Ala Lys Gly	Thr Thr Glu Leu Glu	
350	355	360
Glu Glu Phe Glu Arg Arg Trp Arg Ser Leu	Arg Pro Gly Gly Ser	
365	370	375
Thr Gly Leu Gly Ser Gly Ser Ala Ala Pro	Ala Ala Ala Thr Ala	
380	385	390
Ala Ser Ala Glu Leu Thr Ala Ala Ser Ser	Phe Pro Leu Leu Glu	
395	400	405
Arg Phe Thr Ser Asp Gly Phe His Val Asp	Ser Asp Asp Val Leu	
410	415	420
Thr Val Thr Glu Thr Ser His Gly Leu Asn	Phe Glu Tyr Lys Trp	
425	430	435
Glu Ala Gly Cys Gly Ala Glu Glu Tyr Pro	Pro Ser Gly Ala Ala	
440	445	450
Ser Ser Pro Gly Ser Ala Ala Arg Leu Gln	Glu Leu Cys Ala Pro	
455	460	465
Asp Ser Ser Pro Pro Gly Val Val Pro Val	Leu Ser Ala His Ser	
470	475	480
Pro Ser Val Gly Ser Glu Tyr Phe Ile Arg	Leu Glu Gly Ala Val	
485	490	495
Pro Ala Ala Gly His Asp Pro Asp Cys Ala	Gly Cys Ala Pro Ser	
500	505	510
Pro Gln Ala Val Thr Asp Gln Asp Asn Asn	Ser Glu Glu Ser Thr	
515	520	525
Val Ala Ser Leu Ala Met Glu Pro Leu Leu	Gly His Ala Pro Pro	
530	535	540
Thr Glu Gly Leu Trp Gly Pro Cys Asp His	His Ser His Arg Arg	
545	550	555
Gln Gly Ser Pro Cys Pro Ser Arg Ser Pro	Ser Pro Gly Thr Pro	
560	565	570
Met Leu Pro Ala Glu Asp Ile Asp Trp Gly	Val Ala Thr Phe Cys	
575	580	585
Pro Pro Phe Phe Asp Asp Pro Leu Gly Ala	Ser Pro Ser Gly Ser	
590	595	600
Pro Gly Ala Gln Pro Ser Pro Ser Asp Glu	Glu Pro Glu Glu Gly	
605	610	615
Lys Val Gly Leu Ala Ala Gln Cys Gly His	Trp Ser Ser Asn Met	
620	625	630
Ser Ala Asn Asn Asn Ser Ala Ser Arg Asp	Pro Glu Ser Trp Asp	
635	640	645
Pro Gly Tyr Val Ser Ser Phe Thr Asp Ser	Tyr Arg Asp Asp Cys	
650	655	660
Ser Ser Leu Glu Gln Thr Pro Arg Ala Ser	Pro Glu Val Gly His	
665	670	675
Leu Leu Ser Gln Glu Asp Pro Arg Asp Phe	Leu Pro Gly Leu Val	
680	685	690
Ala Val Ser Pro Gly Gln Glu Pro Ser Arg	Pro Phe Asn Leu Leu	
695	700	705

Pro Leu Cys Pro Ala Lys Gly Leu Ala Pro Ala Ala Cys Leu Ile  
 710 715 720  
 Thr Ser Pro Trp Thr Glu Gly Ala Val Gly Gly Ala Glu Asn Pro  
 725 730 735  
 Ile Val Glu Pro Lys Leu Ala Gln Glu Ala Glu Gly Ser Ala Glu  
 740 745 750  
 Pro Gln Leu Pro Leu Pro Ser Val Pro Ser Pro Ser Cys Glu Gly  
 755 760 765  
 Ala Ser Leu Pro Ser Glu Glu Ala Ser Ala Pro Asp Ile Leu Pro  
 770 775 780  
 Ala Ser Pro Thr Pro Ala Ala Gly Ser Trp Val Thr Val Pro Glu  
 785 790 795  
 Pro Ala Pro Thr Leu Glu Ser Ser Gly Ser Ser Leu Gly Gln Glu  
 800 805 810  
 Ala Pro Ser Ser Glu Asp Glu Asp Thr Thr Glu Ala Thr Ser Gly  
 815 820 825  
 Val Phe Thr Asp Leu Ser Ser Asp Gly Pro His Thr Glu Lys Ser  
 830 835 840  
 Gly Ile Val Pro Ala Leu Arg Ser Leu Gln Lys Gln Val Gly Thr  
 845 850 855  
 Pro Asp Ser Leu Asp Ser Leu Asp Ile Pro Ser Ser Ala Ser Asp  
 860 865 870  
 Gly Gly Cys Glu Val Leu Ser Pro Ser Ala Ala Gly Pro Pro Gly  
 875 880 885  
 Gly Gln Pro Arg Ala Val Asp Ser Gly Tyr Asp Thr Glu Asn Tyr  
 890 895 900  
 Glu Ser Pro Glu Phe Val Leu Lys Glu Ala His Glu Ser Ser Glu  
 905 910 915  
 Pro Glu Ala Phe Gly Glu Pro Ala Ser Glu Gly Glu Ser Pro Gly  
 920 925 930  
 Pro Asp Pro Leu Leu Ser Val Ser Leu Gly Gly Leu Ser Lys Lys  
 935 940 945  
 Ser Pro Tyr Arg Asp Ser Ala Tyr Phe Ser Asp Leu Asp Ala Glu  
 950 955 960  
 Ser Glu Pro Thr Phe Gly Pro Glu Lys His Ser Gly Ile Gln Asp  
 965 970 975  
 Ser Gln Lys Glu Gln Asp Leu Arg Ser Pro Pro Ser Pro Gly His  
 980 985 990  
 Gln Ser Val Gln Ala Phe Pro Arg Ser Ala Val Ser Ser Glu Val  
 995 1000 1005  
 Leu Ser Pro Pro Gln Gln Ser Glu Glu Pro Leu Pro Glu Val Pro  
 1010 1015 1020  
 Arg Pro Glu Pro Leu Gly Ala Gln Gly Pro Val Gly Val Gln Pro  
 1025 1030 1035  
 Val Pro Gly Pro Ser His Ser Lys Cys Phe Pro Leu Thr Ser Val  
 1040 1045 1050  
 Pro Leu Ile Ser Glu Gly Ser Gly Thr Glu Pro Gln Gly Pro Ser  
 1055 1060 1065  
 Gly Gln Leu Ser Gly Arg Ala Gln Gln Gly Gln Met Gly Asn Pro  
 1070 1075 1080  
 Ser Thr Pro Arg Ser Pro Leu Cys Leu Ala Leu Pro Gly His Pro  
 1085 1090 1095  
 Gly Ala Leu Glu Gly Arg Pro Glu Glu Asp Glu Asp Thr Glu Asp  
 1100 1105 1110  
 Ser Glu Glu Ser Asp Glu Glu Leu Arg Cys Tyr Ser Val Gln Glu  
 1115 1120 1125  
 Pro Ser Glu Asp Ser Glu Glu Glu Pro Pro Ala Val Pro Val Val  
 1130 1135 1140  
 Val Ala Glu Ser Gln Ser Ala Arg Asn Leu Arg Ser Leu Leu Lys  
 1145 1150 1155  
 Met Pro Ser Leu Leu Ser Glu Ala Phe Cys Asp Asp Leu Glu Arg

1160	1165	1170
Lys Lys Lys Ala Val Ser Phe Phe Asp Asp	Val Thr Val Tyr Leu	
1175	1180	1185
Phe Asp Gln Glu Ser Pro Thr Arg Glu Thr Gly	Glu Pro Phe Pro	
1190	1195	1200
Ser Thr Lys Glu Ser Leu Pro Thr Phe Leu Glu	Gly Gly Pro Ser	
1205	1210	1215
Ser Pro Ser Ala Thr Gly Leu Pro Leu Arg Ala	Gly His Ser Pro	
1220	1225	1230
Asp Ser Ser Ala Pro Glu Pro Gly Ser Arg	Phe Glu Trp Asp Gly	
1235	1240	1245
Asp Phe Pro Leu Val Pro Gly Lys Ala Ala	Leu Val Thr Glu Leu	
1250	1255	1260
Asp Pro Ala Asp Pro Val Leu Ala Ala	Pro Pro Thr Pro Ala Ala	
1265	1270	1275
Pro Phe Ser Arg Phe Thr Val Ser Pro Thr Pro	Ala Ser Arg Phe	
1280	1285	1290
Ser Ile Thr His Ile Ser Asp Ser Asp Ala Gln	Ser Val Gly Gly	
1295	1300	1305
Pro Ala Ala Gly Ala Gly Gly Arg Tyr Thr Glu Ala		
1310	1315	